SEIRS Type Mathematical Model Simulation (COVID19 Case)

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ABSTRACT

Indonesia is one of the countries hit by COVID19 cases. Data shows that from January 2023 to May 2023, COVID19 cases are still sweeping Indonesia. Data on COVID19 cases in Indonesia on May 30, 2023 showed that 541 patients were confirmed positive with 8 deaths. The data shows that this COVID19 case still needs to be taken seriously and a solution is found. In this study, the authors developed a mathematical model of the spread of COVID19 cases. The mathematical modeling developed is a mathematical model of type SEIRS. In the SEIRS type mathematical model there are four populations including vulnerable population (S), latent population (E), infection population (I), and cured population (R). In the model, it is assumed that the cured population does not recover permanently, but can again suffer from COVID19 caused by other types of viruses. The purpose of developing a mathematical model of the SEIRS type is to determine the behavior of the population in the compartment diagram. Population behavior can be determined by simulating each population in the model. The simulation is performed when the value of the base reproduction number is less than zero and more than zero. Based on the simulations conducted showed that at the time of, the $\boxed{\mathcal{R}_0 < 1}$ number of latent populations and infections decreased towards zero, while at the time of, latent $\boxed{\mathcal{R}_0 > 1}$ population and infection still remained in the model so that the disease did not disappear.

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I. Introduction

Mathematics is a branch of science that has a major role in the development of science and technology. Mathematics can be applied in various fields of science, both in the fields of social education, health, engineering and other fields of science. This is in line with research conducted by [1]–[3]. In this study, the role of mathematics will be applied in health sciences, which is related to cases of disease spread.

Indonesia is one of the countries hit by COVID19 cases. Data shows that from January 2023 to May 2023, COVID19 cases are still sweeping Indonesia. Data on COVID19 cases in Indonesia on May 30, 2023 showed that 541 patients were confirmed positive with a mortality rate of 8 people [4]. The data shows that this COVID19 case still needs to be taken seriously and a solution is found. In this study, the authors developed a mathematical modeling.

The spread of cases COVID19. Some research related to the role of mathematics in the health sector includes: [5]–[9].

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The purpose of developing a mathematical model of the SEIRS type is to determine the behavior of the population in the compartment diagram. Population behavior can be determined by simulating each population in the model. The simulation is performed when the value of the base reproduction number is less than zero and more than zero. The base reproduction number is the epidemic threshold number or value [10]–[13]. The base reproduction number is denoted by $(\mathcal{R}_0)$.

II. Literature Review

A. System of Differential Equations

Differential equations are equations that contain one or more non-free variables and their derivatives to independent variables, while Differential equation systems A collection of n interdependent differential equations between one equation and another equation [14]–[17]. Systems of differential equations can generally be written:

$$\begin{aligned} x_1' &= f_1(t, x_1, x_2, \dots, x_n) \\ x_2' &= f_2(t, x_1, x_2, \dots, x_n) \\ &\vdots \\ x_n' &= f_n(t, x_1, x_2, \dots, x_n). \end{aligned} \tag{1}$$

As for f_i functions that are real values with their variables $t, x_1, x_2, \text{dan } x_n$.

B. Eigen Values and Eigen Vector

Systems of differential equations (1) can be written in the form:

$$x_n' = f(t, x), \quad x \in \mathbb{R}^n \tag{2}$$

If A is a matrix $n \times n$ hence the non-zero vector x di $\mathbb{R}^n$ called the eigenvector of A if Ax equal to the multiplication of a scalar λ by x, i.e.:

$$Ax = \lambda x \tag{3}$$

scalar λ called the eigenvalue of A, and x named eigenvector corresponding to λ [18]–[21].

C. Fixed Point and Fixed-point Stability

Point $\bar{x}$ In systems of differential equations it is said to be a fixed point if the value $f(\bar{x}) = 0$. Furthermore, the stability of a fixed point can be determined from its eigenvalues [22][23]. A fixed point is said to be stable if it satisfies the condition that each real eigenvalue is negative: $\lambda < 0$ for each eigenvalue or complex eigenvalue of the section Re(λ) $<$ 0 for each eigenvalue. A fixed point is said to be unstable if there is at least one positive real eigenvalue: $\lambda > 0$ or there is at least one complex eigenvalue with Re(λ) > 0 [24], [25].

D. Basic Reproduction Number

The baseline reproduction number is the number of new infections caused by one primary infection or in other words the baseline reproductive number is the epidemic threshold. The basic reproduction number conditions are:

1. If $\mathcal{R}_0 < 1$ Then the number of infected populations decreases with each generation so that the disease in the system disappears.
2. If $\mathcal{R}_0 > 1$ Then the number of infected populations increases with each generation so that the disease in the system will plague [26]–[29].

The base reproduction number value is determined using The Next Generation Matrix G [30]. The dominant eigenvalue of the matrix is the value of the base reproduction number. Adapun *The Next Generation Matrix G*:

$$G = FV^{-1}. \tag{4}$$

As for F called the new infection rate matrix with values $F = \frac{\partial F_i}{\partial x_j}(x_0)$, While V matrix of individual displacement rates with values $V = \frac{\partial V_i}{\partial x_j}(x_0)$. Both matrices are evaluated at fixed points (x_0).

III. Methods

A. Data and Data Sources

The data used in this study are secondary data obtained from previous journals, the website of the Ministry of Health of the Republic of Indonesia, and proceedings. In addition, the data in the study also used assumption data both for the number of population and parameter values contained in the mathematical model.

B. Limitations in SEIRS Type Mathematical Models

Some of the limitations contained in the SEIRS mathematical model developed include that in each population there is natural death, there is a constant birth rate, in latent and infectious populations there is natural death, and the nature of healing in the cured population is not permanent.

C. Stages of Research

This research was carried out in several stages, including literature studies by collecting journals related to mathematical modeling, especially those that discuss cases of disease spread, developing mathematical modeling which is the result of education from previous mathematical models, determining fixed points, determining basic reproduction numbers to analyze fixed point stability, and simulations to determine population behavior in modeling.

III. Results and Discussion

A. System of Differential Equations Mathematical Models COVID19 SEIRS Type

$$\begin{aligned}
\frac{dS}{dt} &= \lambda + \pi R - \left(\mu_1 + \rho \frac{I}{N}\right) S \\
\frac{dE}{dt} &= \rho \frac{SI}{N} - (\mu_1 + \mu_2 + \gamma) E \\
\frac{dI}{dt} &= \gamma E - (\mu_1 + \mu_2 + \tau) I \\
\frac{dR}{dt} &= \tau I - (\pi + \mu_1) R
\end{aligned} \tag{5}$$

dengan $S + E + I + R = N$.

B. Fixed Point

Fixed Point Mathematical Model COVID19 SEIRS type there are two, namely a fixed point without disease and a fixed point without disease. Such fixed points are determined using substitution and elimination methods. To determine fixed points is done by creating each raet change population towards time same with zero, formulated as followed: $\frac{dS}{dt} = 0$; $\frac{dE}{dt} = 0$; $\frac{dI}{dt} = 0$; dan $\frac{dR}{dt} = 0$. Based on the analysis carried out, a point is obtained. It remains as follows:

a. Fixed Point Without Disease

$$(S, E, I, R) = \left(\frac{\lambda}{\mu}, 0,0,0\right)$$

b. Fixed Point of Disease

(S^*, E^*, I^*, R^*) with value:

$$S^* = \frac{N(\mu_1+\mu_2+\gamma)(\mu_1+\mu_2+\tau)}{\gamma\rho}$$
$$E^* = \frac{(\mu_1+\pi)(\mu_1+\mu_2+\tau)(\gamma\lambda\rho - N\mu_1(\gamma+\mu_1+\mu_2)(\mu_1+\mu_2+\tau))}{\gamma\rho(\gamma(\mu_1+\mu_2)(\mu_1+\pi)+\gamma\mu_1\tau+(\mu_1+\mu_2)(\mu_1+\pi)(\mu_1+\mu_2+\tau))}$$
$$I^* = \frac{(\mu_1+\pi)(\gamma\lambda\rho - N\mu_1(\gamma+\mu_1+\mu_2)(\mu_1+\mu_2+\tau))}{\rho(\gamma(\mu_1+\mu_2)(\mu_1+\pi)+\gamma\mu_1\tau+(\mu_1+\mu_2)(\mu_1+\pi)(\mu_1+\mu_2+\tau))}$$
$$R^* = \frac{\tau(\gamma\lambda\rho - N\mu_1(\gamma+\mu_1+\mu_2)(\mu_1+\mu_2+\tau))}{\rho(\gamma(\mu_1+\mu_2)(\mu_1+\pi)+\gamma\mu_1\tau+(\mu_1+\mu_2)(\mu_1+\pi)(\mu_1+\mu_2+\tau))}$$

C. Basic Reproduction Number

The basic reproduction number is determined using The *Next Generation Matrix G* method. The equation used to determine the value of the base reproduction number is the equation:

$$\frac{dE}{dt} = \rho\frac{SI}{N} - (\mu_1+\mu_2+\gamma)E \qquad (6)$$
$$\frac{dI}{dt} = \gamma E - (\mu_1+\mu_2+\tau)I$$

Based on the analysis carried out, the values of the basic reproduction number are as follows:

$$\mathcal{R}_0 = \frac{\sqrt{\rho\gamma\lambda}}{\sqrt{N\mu_1(\mu_1+\mu_2+\tau)(\mu_1+\mu_2+\gamma)}} \qquad (7)$$

D. Mathematical Model Simulation COVID19 SEIRS Type

Simulation of the SEIRS Type COVID19 Mathematical Model was carried out to see population behavior both at the time $\mathcal{R}_0 < 1$ and $\mathcal{R}_0 > 1$ using the variable values in Table 1:

Table 1. Variable Value

Variable	Information	Value
N	Total Population	100
S	Vulnerable Populations	70
E	Latent Population	30
I	Infection Population	0
R	Population Cured	0

1. Current population behavior $\mathcal{R}_0 < 1$

Population behavior when $\mathcal{R}_0 < 1$ carried out using variable values in Table 1 and parameter values in Table 2:

Table 2. Current Parameter Value $\mathcal{R}_0 < 1$

Parameter	Information	Value
λ	Birth Rate	0,3
π	The rate of movement of cured populations becomes vulnerable	0,01
μ_1	Natural Death Rate	0,0125
μ_2	Death Rate Due to Disease	0,017

Parameter	Information	Value
ρ	Cash value between infected population and vulnerable population	0,2
γ	Rate of movement of latent populations into infections	0,8
τ	Rate of movement of infected population to cured	0.04

Based on the simulation carried out, the following graph was obtained:

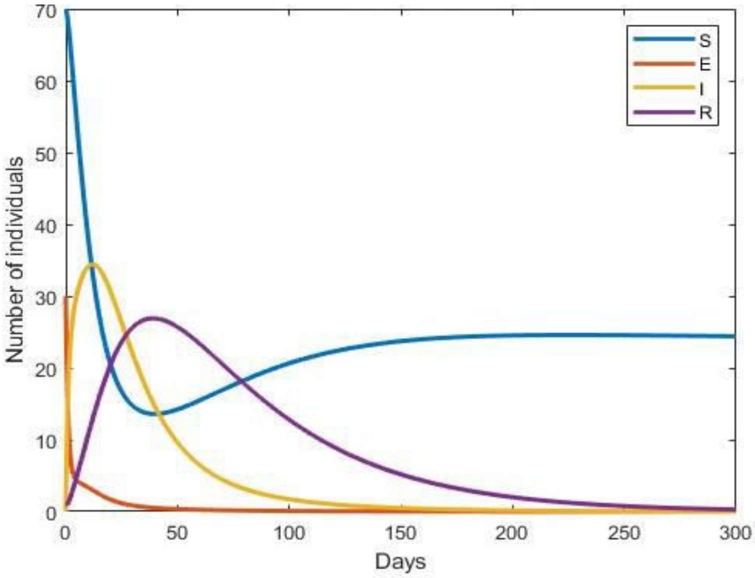

Figure 1. Current population behavior $\mathcal{R}_0 < 1$

The behavior of the population in the mathematical modeling of the SEIRS type when conditions $\mathcal{R}_0 < 1$ can be seen in Figure 1. The graph shows that when the condition of the $\mathcal{R}_0 < 1$ number of latent populations and infected populations decreases towards zero, resulting in the recovered population also decreases. For vulnerable populations, there is an increase caused by latent populations and decreasing infection populations.

2. Current population behavior $\mathcal{R}_0 > 1$

Population behavior when $\mathcal{R}_0 > 1$ performed using the variable values in Table 1 and the parameter values of Table 3:

Table 3. Current Parameter Value $\mathcal{R}_0 > 1$

Parameter	Information	Value
λ	Birth Rate	0,7
π	The rate of movement of cured populations becomes vulnerable	0,01
μ_1	Natural Death Rate	0,01
μ_2	Death Rate Due to Disease	0,007
ρ	Cash value between infected population and vulnerable population	0,3
γ	Rate of movement of latent populations into infections	0,2
τ	Rate of movement of infected population to cured	0.05

Based on the simulation carried out, the following graph was obtained:

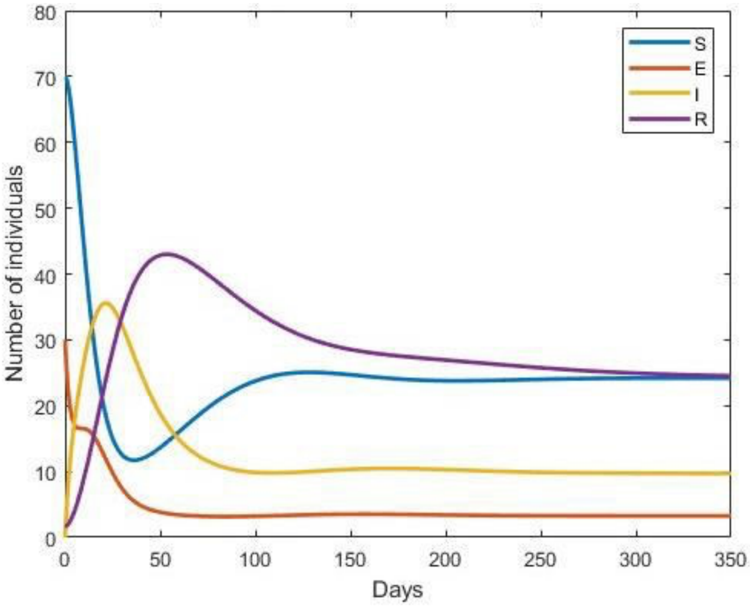

Figure 2. Current Population Behavior $\mathcal{R}_0 > 1$

The behavior of the population in the mathematical modeling of the SEIRS type when conditions $\mathcal{R}_0 > 1$ can be seen in Figure 1. The graph shows that while $\mathcal{R}_0 > 1$ latent and infected populations do not decline to zero, they still exist so that the disease does not disappear.

IV. Conclusion

Based on the analysis and discussion that has been carried out on the SEIRS type mathematical model of COVID19 case, it can be concluded that the mathematical model has two fixed points, namely a fixed point without disease and a fixed point with disease. In addition, the results show that at the time of the $\mathcal{R}_0 > 1$ number of latent populations and infections decreased towards zero, whereas at the time $\mathcal{R}_0 > 1$ of , latent popolation and infection still remained in the model so that the disease did not disappear.

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